We claim:

1. A method for identifying proteins or chemicals that directly or indirectly modulate a genomic polynucleotide comprising:

a) providing a reporter gene integrated into a non-yeast, eukaryotic genome contained in at least one living cell,

b) contacting said cell with a predetermined concentration of a modulator, and detecting reporter gene activity from said at least one living cell,

wherein said reporter gene was integrated into said genome by as adeno-associated viral vector.

2. The method of claim 1, wherein said reporter gene encodes a beta-lactamase.

3. The method of claim 1, wherein said detecting further comprises measuring cleavage of a membrane permeant BL substrate, wherein said membrane permeant BL substrate is transformed in said cell.

4. The method of claim 3, wherein said membrane permeant BL substrate comprises a donor and acceptor.

5. The method of claim 4, wherein said detecting further comprises measuring FRET between said donor and said acceptor.

6. The method of claim 3, wherein said at least one living cell is a mammalian cell.

7. The method of claim 6, wherein said reporter gene randomly integrates into said genome.

8. The method of claim 7, wherein said living cell is contacted with said modulator prior to inserting of said reporter gene in said non-yeast, eukaryotic genome and further comprising the step of determining the coding nucleic acid sequence of a polynucleotide operably linked to said reporter gene, wherein said adeno-associated viral vector construct comprises a splice donor, a splice acceptor and an IRES element.

9. The method of claim 6, wherein said reporter gene encodes cytosolic BL and said cell comprises a receptor that is known to bind said modulator.

10. The method of claim 9, wherein said receptor is a nuclear receptor heterologously expressed by said cell.

11. The method of claim 9, wherein said receptor has a transmembrane domain and is homologously expressed by said cell.

12. The method of claim 11, wherein said modulator is a non-peptide.

13. The method of claim 9, wherein said cell is contacted with a predetermined concentration of a second modulator and detecting reporter gene activity before and after contacting said cell with said second modulator.

14. The method of claim 6, wherein said cell comprises an orphan protein heterologously expressed by said cell.

15. The method of claim 6, wherein said reporter gene activity is increased in the presence of said modulator compared with the reporter gene activity in the absence of said modulator.

16. The method of claim 6, wherein said modulator is known to bind to a receptor expressed by said cell and said reporter gene activity in said cell is increased in the presence of said modulator compared to the reporter gene activity detected from a corresponding cell in the presence of said modulator, wherein said corresponding cell does not express of said receptor.

17. A method of identifying active genomic polynucleotides, comprising:

contacting living cells with a substrate for a product of a reporter gene, and

sorting living cells by fluorescence,

wherein said cells are eukaryotic cells and comprise a genome having a stably integrated reporter gene and said fluorescence indicates reporter gene activity,

wherein said reporter gene was integrated into said genome by an adeno-associated viral vector.

18. The method of claim 17, wherein said sorting further comprises measuring cleavage of a substrate for said reporter gene product by fluorescence spectroscopy in a FACS, wherein said substrate is transformed in said cell.

19. The method of claim 18, wherein said substrate has a donor and acceptor and said measuring further comprises measuring FRET between a donor and an acceptor.

20. The method of claim 18, wherein said sorting further comprises separating said cells without reporter gene activity from said cells with reporter gene activity.

21. The method of claim 20, wherein said cells are contacted with only a cell culture medium in the absence of a test chemical.

22. The method of claim 21, wherein said cells without reporter gene activity are contacted with a test chemical and further sorted by fluorescence for reporter gene activity.

23. The method of claim 22, wherein said test chemical is an agonist.

24. The method of claim 22, wherein said test chemical is an antagonist.

25. The method of claim 22, wherein said cells without reporter gene activity are contacted with a test chemical and further sorted by fluorescence for reporter gene activity.

26. The method of claim 23, wherein said cells with reporter gene activity are contacted with an antagonist and further sorted by fluorescence for reporter gene activity.

27. The method of claim 18, wherein said cells express an identified receptor that binds a modulator known to bind to said identified receptor.

28. The method of claim 27, wherein said living cells comprise a heterologous G-protein.

29. The method of claim 18, wherein said living cells comprise a heterologous protein having a membrane domain.

30. A composition of matter comprising a non-yeast, eukaryotic cell having a genome with a stably integrated reporter gene construct comprising a polynucleotide encoding a protein having a reporter gene activity, an IRES element, a splice donor site and a splice acceptor site, wherein said reporter gene was integrated in said genome by an adeno-associated viral vector.

31. The composition of matter of claim 30, further comprising a heterologous protein expressed in said cell.

32. The composition of matter of claim 31, wherein said cell is a mammalian cell.

33. The composition of matter of claim 32, wherein said polynucleotide contains nucleic acid sequences that are preferred by said mammalian cell for expression.

34. The composition of matter of claim 33, wherein said cell further comprises a reporter gene substrate, wherein said reporter gene substrate is transformed inside said cell by intracellular esterases.

35. The composition of matter of claim 34, wherein said reporter gene encodes a cytosolic beta-lactamase.

36. A method of screening compounds with an active genomic polynucleotide, comprising:

1) optionally contacting a multiclonal population of cells with a first test chemical prior to separating said cells by a FACS,

2) separating by a FACS said multiclonal population of cells into reporter gene expressing cells and non-reporter gene expressing cells, wherein said reporter gene expressing cells have a detectable difference in cellular fluorescence properties compared to non-reporter gene expressing cells, and

Ai) contacting said non-reporter gene expressing cells with a second test chemical, and

Aii) sorting by a FACS said non-reporter gene expressing cells into a) second test chemical activated cells and b) second test chemical non-activated cells,

wherein said second test chemical activated cells have reporter gene activity detectable by a FACS and said second test chemical non-activated cells have no reporter gene activity detectable by FACS, or

Bi) contacting said reporter gene expressing cells with a third test chemical, and

Bii) sorting by a FACS said reporter gene expressing cells into a) third test chemical activated cells and b) third test chemical non-activated cells,

wherein said third test chemical activated cells have reporter gene activity detectable by a FACS and said third test chemical non-activated cells have no reporter gene activity detectable by FACS,

wherein said multiclonal population of cells comprises eukaryotic cells having a reporter gene expression construct integrated into a genome of said eukaryotic cells and a membrane permanent reporter gene substrate transformed inside said cells to a membrane impermeant reporter gene substrate,

wherein said reporter gene was integrated into said genome by an adeno-associated viral vector.

37. The method of claim 36, wherein said reporter gene activity is measured by FRET.

38. The method of claim 36, wherein said steps of Ai and Aii or Bi and Bii are repeated.

39. The method of claim 36, wherein said second test chemical activated cells are washed, then contacted with a modulator in the presence of said second test chemical and tested for reporter gene activity.

40. The method of claim 39, wherein said modulator is present in a concentration of 10 μM or less.

41. The method of claim 36, wherein said eukaryotic cells express a heterologous protein.

42. A method for identifying an expressed protein that directly or indirectly modulates a genomic polynucleotide, comprising: providing at least one living non-yeast, eukaryotic cell comprising a reporter gene that can be under transcriptional control of said at least one living non-yeast, eukaryotic cell's genome and stably integrated into a genomic polynucleotide site, contacting said cell with a predetermined concentration of a known modulator, and detecting reporter gene activity from said at least one living non-yeast, eukaryotic cell; wherein said at least one living non-yeast, eukaryotic cell expresses a heterologous protein and said known modulator increases or decreases the expression of said reporter gene in the presence of said heterologous protein, wherein said reporter gene was integrated into said genome by an adeno-associated viral vector.

43. The method of claim 42, wherein said detecting further comprises measuring cleavage of a reporter gene substrate, wherein said membrane permeant reporter gene substrate is transformed in said at least one living non-yeast, eukaryotic cell.

44. The method of claim 43, wherein said reporter gene substrate has a donor and acceptor in said at least one living non-yeast, eukaryotic cell.

45. The method of claim 44, wherein said method further comprises sorting a population of cells with a FACS.

46. The method of claim 42, wherein said cell is a mammalian cell.

47. The method of claim 46, wherein said reporter gene includes a reporter gene expression construct for random integration into said genome.

48. The method of claim 47, further comprising the step of determining a portion of the coding nucleic acid sequence of a polynucleotide operably linked to said reporter gene expression construct.

49. The method of claim 46, wherein said reporter gene expression construct comprises a cytosolic reporter gene product, said construct comprises a splice donor, a splice acceptor and an IRES element and said cell comprises a receptor that is known to bind said known modulator.

50. The method of claim 46, wherein said hetereologous protein is selected from the group consisting of hormone receptors, intracellular receptors, receptors of the cytokine superfamily, G-protein coupled receptors, heterologous G-proteins, neurotransmitter receptors, and tyrosine kinase receptors.

51. The method of claim 46, wherein said hetereologous protein has a transmembrane domain.

52. The method of claim 51, further comprising over expressing said heterologous protein.

53. The method of claim 46, wherein said at least one living non-yeast, eukaryotic cell is contacted with a predetermined concentration of a second modulator and detecting β-lactamase activity after contacting said cell with said known modulator.

54. The method of claim 46, wherein said cell comprises an orphan protein heterologously expressed by said at least one living non-yeast, eukaryotic cell.

55. The method of claim 46, wherein said reporter gene activity is increased in the presence of said modulator compared to the absence of said modulator.

56. The method of claim 46, wherein said known modulator is known to bind to a receptor and said reporter gene activity in said at least one living non-yeast, eukaryotic cell is increased in the presence of said modulator compared to the reporter gene activity detected from a corresponding cell in the presence of said known modulator, wherein said corresponding cell does not express said heterologous protein.

57. A method for identifying modulators, comprising:

a) contacting at least one living mammalian cell with a test chemical at a predetermined concentration and a known modulator at a predetermined concentration, wherein said at least one living mammalian cell comprises a reporter gene polynucleotide that can be under transcriptional control of said at least one living mammalian cell's genome and stably integrated into a genomic polynucleotide site, and

b) detecting expression of said reporter gene by said at least one living mammalian cell, wherein said known modulator increases or decreases expression of said reporter gene located at said genomic polynucleotide site, wherein said reporter gene was integrated into said genome using an adeno-associated viral vector.

58. The method of claim 57, wherein said test chemical changes expression of said -lactamase polynucleotide by said known modulator.

59. The method of claim 57, wherein said -lactamase polynucleotide further comprises a splice acceptor site.

60. The method of claim 59, wherein said reporter gene construct further comprises an IRES.

61. The method of claim 58, wherein said test chemical or known modulator is provided at a concentration less than about 1microM.

62. The method of claim 57, further comprising separating a population of living mammalian cells into 1) a population of living mammalian cells that expresses β-lactamase and 2) a population of living mammalian cells that does not express β-lactamase.

63. The method of claim 61, wherein said separating further comprises measuring cleavage of a membrane permeant β-lactamase substrate in said population of living mammalian cells by fluorescence spectroscopy in a FACS, wherein the fluorescence of said membrane permeant β-lactamase substrate is transformed by β-lactamase in at least one living mammalian cell.

64. The method of claim 57, wherein said known modulator modulates a receptor selected from the group consisting of intracellular receptors and G-protein coupled receptors.

65. The method of claim 64, wherein said known modulator is an agonist.

66. The method of claim 64, wherein said known modulator is an antagonist.

67. The method of claim 65, wherein said known modulator is contacted with said at least one living mammalian cell prior to contacting said test chemical with said at least one living mammalian cell.

68. The method of claim 57, wherein said test chemical is a modulator for a protein selected from the group consisting of hormone receptors, intracellular receptors, receptors of the cytokine superfamily, G-protein coupled receptors, heterologous G-proteins, neurotransmitter receptors, and tyrosine kinase receptors.

69. The method of claim 57, wherein said at least one living mammalian cell further comprises a heterologously expressed protein selected from the group consisting of hormone receptors, intracellular receptors, signaling molecules, receptors of the cytokine superfamily, G-protein coupled receptors, heterologous G-proteins, neurotransmitters, and tyrosine kinase receptors.

70. The method of claim 69, wherein said heterologously expressed protein is a G-protein coupled receptor or a heterologous G-protein.

71. The method of claim 57, further comprising the step of activating said at least one living mammalian cell with a G-protein coupled receptor modulator.

72. The method of claim 71, wherein said at least one living mammalian cell further comprises an orphan receptor.

73. The method of claim 57, wherein said at least one living mammalian cell is of cell type from a panel of different cell types and steps (a) and (b) are performed on each cell type.

74. The method of claim 57, wherein said genomic polynucleotide site is part of a gene not known to be modulated by said known modulator.

75. The method of claim 74, wherein said known modulator is as an agonist.

76. The method of claim 75, wherein said test chemical is an antagonist.

77. The method of claim 74, wherein said known modulator is an antagonist.

78. The method of claim 77, wherein said test chemical is an agonist.

79. A method for identifying a modulator, comprising:

a) contacting a population of non-yeast, eukaryotic cells with a test chemical and a known modulator, wherein said population of non-yeast, eukaryotic cells comprises a genome with a stably integrated reporter gene, comprising:

1) a polynucleotide encoding a protein having reporter gene activity, and

2) a splice acceptor site; and

b) detecting the activity of said reporter gene expressed by said population of non-yeast, eukaryotic cells, wherein said known modulator increases or decreases the expression of said polynucleotide encoding a protein having reporter gene activity, and said known modulator modulates a biological process or target, wherein said reporter gene was integrated into said genome by an adeno-associated viral vector.

80. The method of claim 79, wherein said reporter gene expression construct further comprises a splice donor site.

81. The method of claim 80, wherein said reporter gene expression construct further comprises an IRES element.

82. The method of claim 79, wherein said population of non-yeast, eukaryotic cells further comprises an expressed heterologous G-protein coupled receptor.

83. The method of claim 82, wherein said population of non-yeast, eukaryotic cells further comprises an orphan G-protein coupled receptor.

84. A method for identifying a ligand of a target, comprising: contacting a eukaryotic cell with a test chemical at a predetermined concentration, wherein said eukaryotic cell comprises 1) a genomic polynucleotide with a reporter gene expression construct under expression control by a first polynucleotide in said genomic polynucleotide and 2) a target that does not normally modulate transcription of a gene product under expression control of said first polynucleotide with proviso that said target can directly or indirectly alter expression of said reporter gene expression construct under expression control by said first polynucleotide, and

determining expression of said reporter gene expression construct, wherein said reporter gene was integrated into said genome by an adeno-associated viral vector.

85. The method of claim 84, wherein said eukaryotic cell is a mammalian cell.

86. The method of claim 85, wherein said target is a heterologously expressed protein.

87. The method of claim 86, wherein said heterologously expressed protein is a membrane protein.

88. The method of claim 85, wherein said heterologously expressed protein is a GPCR.

89. The method of claim 85, wherein said heterologously expressed protein is an ion channel.

90. The method of claim 85, further comprising contacting a eukaryotic cell with a test chemical at a predetermined concentration, wherein said eukaryotic cell comprises 1) a genomic polynucleotide with a reporter gene expression construct under expression control by a first polynucleotide in said genomic polynucleotide and 2) a target that does not normally modulate transcription of a gene product under expression control of said first polynucleotide.

91. The method of claim 85, wherein said gene product is normally expressed in a first tissue and said target is normally expressed in a second tissue, wherein said first tissue is of a different embryonic origin than said second tissue.

92. The method of claim 85, wherein said gene product is normally expressed in a first cell in vivo and said target is normally expressed in a second cell in vivo, wherein said first cell is a different cell type than said second cell.

93. The method of claim 85, wherein expression of said gene product is normally repressed and said target does not increase expression of said gene product in vivo in naturally occurring cells.

94. The method of claim 85, wherein said gene product is normally expressed in a first cell *in vivo* and said target is normally expressed in a second cell *in vivo*, wherein said first cell is a different cell type than said second cell.

95. 'The method of claim 85, wherein expression of said gene product in said eukaryotic cell is not detectable in the absence of said target and said eukaryotic cell does not express detectable levels of protein of said target in the absence of heterologous expression of said target.

96. The method of claim 85, wherein native protein of said gene product and native protein of said target are not expressed in detectable levels in a single, naturally occurring cell.

97. The method of claim 85, wherein native protein of said target in a naturally occurring cell does not modulate expression of native protein of said gene product in said naturally occurring cell.

98. A method for identifying a cellular function of an orphan protein, comprising:

contacting a eukaryotic cell with a test chemical at a predetermined concentration, wherein said eukaryotic cell comprises 1) a genomic polynucleotide with a reporter gene expression construct under expression control by a first polynucleotide in said genomic polynucleotide and 2) an orphan protein,

determining expression of said reporter gene expression construct, and

identifying the function of said genomic polynucleotide with said reporter gene expression construct or its corresponding gene where said reporter gene expression construct has integrated, wherein said reporter gene was integrated into said genome by an adeno-associated viral vector.

99. The method of claim 98, wherein said eukaryotic cell is a mammalian cell.

100. The method of claim 99, wherein said orphan is a heterologously expressed protein.

101. The method of claim 100, wherein said heterologously expressed orphan protein has putative transmembrane domain.

102. The method of claim 99, wherein said heterologously expressed orphan protein is homologous to a GPCR of known function and is overexpressed.

103. A method for identifying a modulator of an orphan protein, comprising:

contacting a eukaryotic cell with a test chemical at a predetermined concentration, wherein said eukaryotic cell comprises 1) a genomic polynucleotide with a reporter gene expression construct under expression control by a first polynucleotide in said genomic polynucleotide and 2) a orphan protein that modulates expression of said reporter gene expression construct, and

determining expression of said reporter gene expression construct, wherein said reporter gene was integrated into said genome by an adeno-associated viral vector.

104. The method of claim 103, wherein said eukaryotic cell is a mammalian cell.

105. The method of claim 104, wherein said orphan protein is a heterologously expressed protein.

106. The method of claim 103, wherein said heterologously expressed orphan protein has putative transmembrane domain.

107. The method of claim 103, wherein said heterologously expressed orphan protein is over expressed and is homologous to a GPCR of known function.

108. A method for identifying intracellular pathways, comprising:

expressing a protein of interest in a plurality of eukaryotic cells, wherein each eukaryotic cell comprises a genomic polynucleotide with a reporter gene expression construct under expression control by a polynucleotide in said genomic polynucleotide, and said plurality of cells has a plurality of integration sites where said reporter gene expression construct has integrated into said genome of each said eukaryotic cell,

optionally contacting said plurality of eukaryotic cells with a ligand of said protein of interest,

determining expression from said reporter gene expression construct, and

identifying said polynucleotide if said expressing of said protein of interest alters expression from said reporter gene expression construct or if said contacting said ligand of said protein of interest alters expression from said reporter gene expression construct,

wherein alteration of said expression from said reporter gene expression construct indicates participation of said protein of interest in an intracellular signaling pathway. wherein said reporter gene was integrated into said genome by an adeno-associated viral vector.

109. The method of claim 108, wherein said eukaryotic cell is a mammalian cell.

110. The method of claim 109, wherein said protein of interest is a heterologously expressed protein and has a known ligand.

111. The method of claim 109, wherein said protein of interest is a heterologously expressed protein and has no known ligand.

112. The method of claim 110, further comprising isolating a eukaryotic cell from said plurality of eukaryotic cells and characterizing said polynucleotide.

113. The method of claim 110, wherein each said eukaryotic cell in said plurality of eukaryotic cells is an isolated, clonal population of cells.

114. The method of claim 113, wherein said plurality of cells comprises at least 10,000 isolated clonal populations of cells.

115. A method for determining a cellular response profile for a target, comprising:

expressing a protein of interest in a plurality of eukaryotic cells, wherein each eukaryotic cell comprises a genomic polynucleotide with a reporter gene expression construct under expression control by a polynucleotide in said genomic polynucleotide, and said plurality of cells has a plurality of integration sites where said reporter gene expression construct has integrated into said genome of each said eukaryotic cell,

optionally contacting said plurality of eukaryotic cells with a ligand of said protein of interest,

determining expression from said β-lactamase expression constructs, and

identifying plurality of said polynucleotides exhibiting a increase, decrease or no change in expression from said β-lactamase expression that results from either said expressing of said protein of interest or said contacting of said ligand,

wherein an increase, decrease or no change in expression of each said polynucleotide from said plurality of polynucleotides indicates a profile of cellular response relating to said protein of interest, wherein said reporter gene was integrated into said genome by an adeno-associated viral vector.

116. A method for determining a cellular response profile for a chemical, comprising:

expressing a protein of interest in a plurality of eukaryotic cells, wherein each eukaryotic cell comprises a genomic polynucleotide with a reporter gene expression construct under expression control by a polynucleotide in said genomic polynucleotide, and said plurality of cells has a plurality of integration sites where said reporter gene expression construct has integrated into said genome of each said eukaryotic cell,

optionally contacting said plurality of eukaryotic cells with a ligand of said protein of interest,

contacting said plurality of eukaryotic cells with a test chemical at a predetermined concentration, and

determining expression from said reporter gene expression constructs, and

identifying plurality of said polynucleotides exhibiting a increase, decrease or no change in expression from said reporter gene expression that results from either said expressing of said protein of interest or said contacting of said ligand,

wherein an increase, decrease or no change in expression of each said polynucleotide from said plurality of polynucleotides indicates a profile of cellular response relating to said test chemical, wherein said reporter gene was integrated into said genome by an adeno-associated viral vector.

117. A method for identifying a modulator of a viral component, comprising:

contacting a eukaryotic cell with a test chemical at a predetermined concentration, wherein said eukaryotic cell comprises 1) a genomic polynucleotide with a reporter gene expression construct under expression control by a first polynucleotide in said genomic polynucleotide and 2) a viral component is not previously known to modulate transcription of a gene product under expression control of said first polynucleotide and said viral component is not an oncogene or proto-oncogene or protein product thereof, and

determining expression of said reporter gene expression construct, wherein said reporter gene was integrated into said genome by an adeno-associated viral vector.

118. The method of claim 117, wherein said viral component is selected from the list consisting of a virus, a capsule, a viral polynucleotide, or a viral protein.

119. The method of claim 118, further comprising contacting a second eukaryotic cell with said test chemical at a predetermined concentration, wherein said eukaryotic cell comprises 1) a second genomic polynucleotide with a reporter gene expression construct under expression control by a second polynucleotide in said second genomic polynucleotide and 2) said viral component, and

determining expression of said reporter gene expression construct, wherein said viral component is selected from the list consisting of a virus, a capsule, a viral polynucleotide, or a viral protein.

120. The method of claim 119, wherein said second eukaryotic cell is from a population of eukaryotic cells, each said eukaryotic cell comprising 1) a genomic polynucleotide with a reporter gene expression construct and 2) said viral component.

121. A method for identifying a cellular function of a viral component, comprising:

contacting a eukaryotic cell with a viral component at a predetermined concentration or expressing a viral component in said eukaryotic cell, wherein said eukaryotic cell comprises 1) a genomic polynucleotide with a reporter gene expression construct under expression control by a first polynucleotide in said genomic polynucleotide,

optionally contacting said eukaryotic cell with a second viral component of a virus that is different from said viral component,

determining expression of said reporter gene expression construct, and

identifying the function of said genomic polynucleotide with said reporter gene expression construct or gene where said reporter gene expression construct has integrated, wherein said reporter gene was integrated into said genome by an adeno-associated viral vector.

122. A method for identifying a chemical that modulates a physiological response or cellular pathway, comprising:

contacting a eukaryotic cell with a test chemical at a predetermined concentration, wherein said eukaryotic cell comprises 1) a genomic polynucleotide with a reporter gene expression construct under expression control by a first polynucleotide in said genomic polynucleotide, wherein said cell is characterized as comprising a physiological response of interest or a cellular pathway of interest, and

contacting said eukaryotic cell with a signal molecule, and

determining expression of said reporter gene expression construct, wherein said reporter gene was integrated into said genome by an adeno-associated viral vector.

123. The method of claim 122, said signal molecule is a naturally occurring molecule that binds to the outside of said eukaryotic cell and said eukaryotic cell is a mammalian cell.

124. The method of claim 123, said physiological response occurs in vivo in an cell selected from the group consisting of a nerve cell, cardiac cell, epithelial cell, muscle cell, endocrine cell, paracrine cell, blood cell, and connective tissue cell.

125. The method of claim 122, wherein said signal molecule increases expression.

126. The method of claim 125, wherein said polynucleotide has a gene product that does not alter said cellular pathway or physiological response.

127. A chemical identified by any of the above methods for identifying useful chemicals.

128. A method for identifying and developing a drug, comprising:

1) contacting a population of non-yeast, eukaryotic cells with a test chemical and a known modulator, wherein said population of non-yeast, eukaryotic cells comprises a genome with a stably integrated reporter gene expression construct, comprising:

a) a polynucleotide encoding a protein having reporter gene activity, and

b) a splice acceptor site; and

2) detecting expression of said reporter gene polynucleotide expressed by said population of non-yeast, eukaryotic cells, wherein said known modulator increases or decreases the expression of said polynucleotide encoding a protein having β-lactamase activity, and said known modulator modulates a biological process or target,

3) determining whether said test chemical alters expression of said reporter gene polynucleotide,

4) optionally testing for toxic effects of said test chemical in a cell-based assay,

5) optionally generating a second test chemical based on the structure-property relationships of said test chemical,

6) optionally determining whether said second test chemical alters expression of said β-lactamase polynucleotide,

7) testing for toxic effects of said test chemical or said second test chemical in a mammal, and

8) testing for therapeutic effects of said test chemical or said second test chemical in a mammal,

wherein said reporter gene was integrated into said genome by an adeno-associated viral vector.

129. A drug chemical identified and developed by the following method, comprising:

1) contacting a population of non-yeast, eukaryotic cells with a test chemical and a known modulator, wherein said population of non-yeast, eukaryotic cells comprises a genome with a stably integrated reporter gene expression construct, comprising:

a) a polynucleotide encoding a protein having reporter gene activity, and

b) a splice acceptor site; and

2) detecting expression of said reporter gene polynucleotide expressed by said population of non-yeast, eukaryotic cells, wherein said known modulator increases or decreases the expression of said polynucleotide encoding a protein having reporter gene activity, and said known modulator modulates a biological process or target,

3) determining whether said test chemical alters expression of said reporter gene,

4) optionally testing for toxic effects of said test chemical in a cell-based assay,

5) optionally generating a second test chemical based on the structure-property relationships of said test chemical,

1) optionally determining whether said second test chemical alters expression of said reporter gene,

2) testing for toxic effects of said test chemical or said second test chemical in a mammal, and

3) testing for therapeutic effects of said test chemical or said second test chemical in a mammal,

wherein said reporter gene was integrated into said genome by an adeno-associated viral vector

130. The drug of claim 129, wherein said drug can be used to treat a medical condition selected from the group consisting of immune response, cardiac disfunctions and disease, vascular disfunctions and diseases, neural disfunctions and disease, endocrine disfunctions and disease, gastro-intestinal disfunctions and disease, obesity, diabetes, inflammation disfunctions and disease, cancer and trauma.

131. A pharmaceutical composition, comprising a therapeutic agent and a pharmaceutically acceptable carrier.

132. The pharmaceutical composition of claim 130, said therapeutic agent having the structure of Chemical A or B and said pharmaceutically acceptable carrier is selected for treating undesired T-cell activation or an undesired immune response.

133. An adeno-associated viral vector for integration into a genome, comprising:
a nucleic acid molecule encoding a splice acceptor sequence, a reporter gene, and a splice donor sequence, wherein said reporter gene is to be under expression control of said genome.

134. The adeno-associated viral vector of claim 133,
wherein said reporter gene comprises a nucleic acid molecule encodes a beta-lactamase.

135. The adeno-associated viral vector claim 133,
further comprising an ATG sequence.

136. The adeno-associated viral vector of claim 135,
further comprising a Kozak's sequence.

137. The adeno-associated viral vector of claim 133,
further comprising an internal ribosome entry site.

138. The adeno-associated viral vector of claim 133,
further comprising a poly-adenylation site.

139. The adeno-associated viral vector of claim 133,
further comprising at least one inverted terminal repeat sequence.

140. The adeno-associated viral vector of claim 139,
wherein said splice acceptor sequence, said reporter gene, and said splice donor sequence are oriented in a 5' to 3' direction between two inverted terminal repeat sequences.

141. The adeno-associated viral vector of claim 133,
wherein said vector lacks a promoter to express said reporter gene.

142. The adeno-associated viral vector of claim 133,
wherein said vector lacks a promoter to express said reporter gene.

143. The adeno-associated viral vector of claim 139,
wherein said nucleic acid molecule comprises a splice acceptor sequence operably linked to reporter gene, which is operably linked to a selectable maker, which is operably linked to a splice donor sequence.